We claim

1. The use of a nucleic acid having promoter activity, comprising

   A) the nucleic acid sequence SEQ. ID. NO. 1 or
   B) a sequence derived from this sequence by substitution, insertion or deletion of nucleotides and having an identity of at least 90% at the nucleic acid level with the sequence SEQ. ID. NO. 1,
   or
   C) a nucleic acid sequence which hybridizes with the nucleic acid sequence SEQ. ID. NO. 1 under stringent conditions, or
   D) functionally equivalent fragments of the sequences of A), B) or C)

   for the transcription of genes.

2. The use of an expression unit comprising a nucleic acid having promoter activity according to claim 1, and additionally functionally linked a nucleic acid sequence which ensures the translation of ribonucleic acids, for the expression of genes.

3. The use according to claim 2, wherein the expression unit comprises:

   E) the nucleic acid sequence SEQ. ID. NO. 2 or
   F) a sequence derived from this sequence by substitution, insertion or deletion of nucleotides and having an identity of at least 90% at the nucleic acid level with the sequence SEQ. ID. NO. 2, or
   G) a nucleic acid sequence which hybridizes with the nucleic acid sequence SEQ. ID. NO. 2 under stringent conditions, or
   H) functionally equivalent fragments of the sequences of E), F) or G).

4. The use according to claim 3, wherein the expression unit consists of a nucleic acid of sequence SEQ. ID. NO. 2.

5. A nucleic acid having promoter activity, comprising

   A) the nucleic acid sequence SEQ. ID. NO. 1 or
   B) a sequence derived from this sequence by substitution, insertion or deletion of nucleotides and having an identity of at least 90% at the nucleic acid level with the sequence SEQ. ID. NO. 1,
   or

C) a nucleic acid sequence which hybridizes with the nucleic acid sequence SEQ. ID. NO. 1 under stringent conditions, or
D) functionally equivalent fragments of the sequences of A), B) or C),

with the proviso that the nucleic acid having the sequence SEQ. ID. NO. 1 is excluded.

6. An expression unit comprising a nucleic acid having promoter activity according to claim 5 and additionally functionally linked nucleic acid sequence which ensures the translation of ribonucleic acids.

7. An expression unit according to claim 6, comprising

E) the nucleic acid sequence SEQ. ID. NO. 2 or
F) a sequence derived from this sequence by substitution, insertion or deletion of nucleotides and having an identity of at least 90% at the nucleic acid level with the sequence SEQ. ID. NO. 2, or
G) a nucleic acid sequence which hybridizes with the nucleic acid sequence SEQ. ID. NO. 2 under stringent conditions, or
H) functionally equivalent fragments of the sequences of E), F) or G),

with the proviso that the nucleic acid having the sequence SEQ. ID. NO. 2 is excluded.

8. A method for altering or causing the transcription rate of genes in microorganisms compared with the wild type by

a) altering the specific promoter activity in the microorganism of endogenous nucleic acids having promoter activity according to claim 1, which regulate the transcription of endogenous genes, compared with the wild type or

b) regulating the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 1 or by nucleic acids having promoter activity according to claim 1 with altered specific promoter activity according to embodiment a), where the genes are heterologous in relation to the nucleic acids having promoter activity.

9. The method according to claim 8, wherein the regulation of the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 1 or by nucleic acids having promoter activity according to

claim 1 with altered specific promoter activity according to embodiment a) is achieved by

b1) introducing one or more nucleic acids having promoter activity according to claim 1, where appropriate with altered specific promoter activity, into the genome of the microorganism so that transcription of one or more endogenous genes takes place under the control of the introduced nucleic acid having promoter activity according to claim 1, where appropriate with altered specific promoter activity, or

b2) introducing one or more genes into the genome of the microorganism so that transcription of one or more of the introduced genes takes place under the control of the endogenous nucleic acids having promoter activity according to claim 1, where appropriate with altered specific promoter activity, or

b3) introducing one or more nucleic acid constructs comprising a nucleic acid having promoter activity according to claim 1, where appropriate with altered specific promoter activity, and functionally linked one or more nucleic acids to be transcribed, into the microorganism.

10. The method according to claim 8 or 9, wherein to increase or cause the transcription rate of genes in microorganisms compared with the wild type

ah) the specific promoter activity in the microorganism of endogenous nucleic acids having promoter activity according to claim 1, or which regulate the transcription of endogenous genes, is increased compared with the wild type, or

bh) the transcription of genes in the microorganism is regulated by nucleic acids having promoter activity according to claim 1 or by nucleic acids having increased specific promoter activity according to embodiment a), where the genes are heterologous in relation to the nucleic acids having promoter activity.

11. The method according to claim 10, wherein the regulation of the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 1 or by nucleic acids having promoter activity according to claim 1 with increased specific promoter activity according to embodiment a) is

achieved by

bh1) introducing one or more nucleic acids having promoter activity according to claim 1, where appropriate with increased specific promoter activity, into the genome of the microorganism so that transcription of one or more endogenous genes takes place under the control of the introduced nucleic acid having promoter activity according to claim 1, where appropriate with increased specific promoter activity, or

bh2) introducing one or more genes into the genome of the microorganism so that transcription of one or more of the introduced genes takes place under the control of the endogenous nucleic acids having promoter activity according to claim 1, where appropriate with increased specific promoter activity, or

bh3) introducing one or more nucleic acid constructs comprising a nucleic acid having promoter activity according to claim 1, where appropriate with increased specific promoter activity, and functionally linked one or more nucleic acids to be transcribed, into the microorganism.

12. The method according to claim 8 or 9, wherein to reduce the transcription rate of genes in microorganisms compared with the wild type

ar) the specific promoter activity in the microorganism of endogenous nucleic acids having promoter activity according to claim 1, which regulate the transcription of endogenous genes, is reduced compared with the wild type, or

br) nucleic acids having reduced specific promoter activity according to embodiment a) are introduced into the genome of the microorganism so that the transcription of endogenous genes takes place under the control of the introduced nucleic acid having reduced promoter activity.

13. A method for altering or causing the expression rate of a gene in microorganisms compared with the wild type by

c) altering the specific expression activity in the microorganism of endogenous expression units according to claim 2 or 3, which regulate the expression of the endogenous genes, compared with the wild type or

d) regulating the expression of genes in the microorganism by expression units according to claim 2 or 3 or by expression units according to claim 2 or 3 with altered specific expression activity according to embodiment c), where the genes are heterologous in relation to the expression units.

14. The method according to claim 13, wherein the regulation of the expression of genes in the microorganism by expression units according to claim 2 or 3 or by expression units according to claim 2 or 3 with altered specific expression activity according to embodiment a) is achieved by

d1) introducing one or more expression units according to claim 2 or 3, where appropriate with altered specific expression activity, into the genome of the microorganism so that expression of one or more endogenous genes takes place under the control of the introduced expression units, or

d2) introducing one or more genes into the genome of the microorganism so that expression of one or more of the introduced genes takes place under the control of the endogenous expression units according to claim 2 or 3, where appropriate with altered specific expression activity, or

d3) introducing one or more nucleic acid constructs comprising an expression unit according to claim 2 or 3, where appropriate with altered specific expression activity, and functionally linked one or more nucleic acids to be expressed, into the microorganism.

15. The method according to claim 13 or 14, wherein to increase or cause the expression rate of a gene in microorganisms compared with the wild type

ch) the specific expression activity in the microorganism of endogenous expression units according to claim 2 or 3, which regulate the expression of the endogenous genes, is increased compared with the wild type, or

dh) the expression of genes in the microorganism is regulated by expression units according to claim 2 or 3 or by expression units according to claim 2 or 3 with increased specific expression activity according to embodiment a), where the genes are heterologous in relation to the expression units.

16. The method according to claim 15, wherein the regulation of the expression of genes in the microorganism by expression units according to claim 2 or 3 or by expression units according to claim 2 or 3 with increased specific expression

activity according to embodiment a) is achieved by

dh1) introducing one or more expression units according to claim 2 or 3, where appropriate with increased specific expression activity, into the genome of the microorganism so that expression of one or more endogenous genes takes place under the control of the introduced expression units, where appropriate with increased specific expression activity, or

dh2) introducing one or more genes into the genome of the microorganism so that expression of one or more of the introduced genes takes place under the control of the endogenous expression units according to claim 2 or 3, where appropriate with increased specific expression activity, or

dh3) introducing one or more nucleic acid constructs comprising an expression unit according to claim 2 or 3, where appropriate with increased specific expression activity, and functionally linked one or more nucleic acids to be expressed, into the microorganism.

17. The method according to claim 13 or 14, wherein to reduce the expression rate of genes in microorganisms compared with the wild type

cr) the specific expression activity in the microorganism of endogenous expression units according to claim 2 or 3, which regulate the expression of the endogenous genes, is reduced compared with the wild type, or

dr) expression units with reduced specific expression activity according to embodiment cr) are introduced into the genome of the microorganism so that expression of endogenous genes takes place under the control of the introduced expression units with reduced expression activity.

18. The method according to any of claims 8 to 17, wherein the genes are selected from the group of nucleic acids encoding a protein from the biosynthetic pathway of proteinogenic and non-proteinogenic amino acids, nucleic acids encoding a protein from the biosynthetic pathway of nucleotides and nucleosides, nucleic acids encoding a protein from the biosynthetic pathway of organic acids, nucleic acids encoding a protein from the biosynthetic pathway of lipids and fatty acids, nucleic acids encoding a protein from the biosynthetic pathway of diols, nucleic acids encoding a protein from the biosynthetic pathway of carbohydrates, nucleic acids encoding a protein from the biosynthetic pathway of aromatic compounds, nucleic acids encoding a protein

from the biosynthetic pathway of vitamins, nucleic acids encoding a protein from the biosynthetic pathway of cofactors and nucleic acids encoding a protein from the biosynthetic pathway of enzymes, where the genes may optionally comprise further regulatory elements.

19. The method according to claim 18, wherein the proteins from the biosynthetic pathway of amino acids are selected from the group of aspartate kinase, aspartate-semialdehyde dehydrogenase, diaminopimelate dehydrogenase, diaminopimelate decarboxylase, dihydrodipicolinate synthetase, dihydrodipicolinate reductase, glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, pyruvate carboxylase, triosephosphate isomerase, transcriptional regulator LuxR, transcriptional regulator LysR1, transcriptional regulator LysR2, malate-quinone oxidoreductase, glucose-6-phosphate deydrogenase, 6-phosphogluconate dehydrogenase, transketolase, transaldolase, homoserine O-acetyltransferase, cystathionine gamma-synthase, cystathionine beta-lyase, serine hydroxymethyltransferase, O-acetylhomoserine sulfhydrylase, methylenetetrahydrofolate reductase, phosphoserine aminotransferase, phosphoserine phosphatase, serine acetyl-transferase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine exporter carrier, threonine dehydratase, pyruvate oxidase, lysine exporter, biotin ligase, cysteine synthase I, cysteine synthase II, coenzyme B12-dependent methionine synthase, coenzyme B12-independent methionine synthase, sulfate adenylyltransferase subunit 1 and 2, phosphoadenosine-phosphosulfate reductase, ferredoxin-sulfite reductase, ferredoxin NADP reductase, 3-phosphoglycerate dehydrogenase, RXA00655 regulator, RXN2910 regulator, arginyl-tRNA synthetase, phosphoenolpyruvate carboxylase, threonine efflux protein, serine hydroxymethyltransferase, fructose-1,6-bisphosphatase, protein of sulfate reduction RXA077, protein of sulfate reduction RXA248, protein of sulfate reduction RXA247, protein OpcA, 1-phosphofructokinase and 6-phosphofructokinase.

20. An expression cassette comprising

a) at least one expression unit according to claim 2 or 3 and

b) at least one further nucleic acid to be expressed, and

c) where appropriate further genetic control elements,

where at least one expression unit and a further nucleic acid sequence to be

expressed are functionally linked together, and the further nucleic acid sequence to be expressed is heterologous in relation to the expression unit.

21. The expression cassette according to claim 20, wherein the further nucleic acid sequence to be expressed is selected from the group of nucleic acids encoding a protein from the biosynthetic pathway of proteinogenic and non-proteinogenic amino acids, nucleic acids encoding a protein from the biosynthetic pathway of nucleotides and nucleosides, nucleic acids encoding a protein from the biosynthetic pathway of organic acids, nucleic acids encoding a protein from the biosynthetic pathway of lipids and fatty acids, nucleic acids encoding a protein from the biosynthetic pathway of diols, nucleic acids encoding a protein from the biosynthetic pathway of carbohydrates, nucleic acids encoding a protein from the biosynthetic pathway of aromatic compounds, nucleic acids encoding a protein from the biosynthetic pathway of vitamins, nucleic acids encoding a protein from the biosynthetic pathway of cofactors and nucleic acids encoding a protein from the biosynthetic pathway of enzymes.

22. The expression cassette according to claim 21, wherein the proteins from the biosynthetic pathway of amino acids are selected from the group of aspartate kinase, aspartate-semialdehyde dehydrogenase, diaminopimelate dehydrogenase, diaminopimelate decarboxylase, dihydrodipicolinate synthetase, dihydrodipicolinate reductase, glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, pyruvate carboxylase, triosephosphate isomerase, transcriptional regulator LuxR, transcriptional regulator LysR1, transcriptional regulator LysR2, malate-quinone oxidoreductase, glucose-6-phosphate deydrogenase, 6-phosphogluconate dehydrogenase, transketolase, transaldolase, homoserine O-acetyltransferase, cystathionine gamma-synthase, cystathionine beta-lyase, serine hydroxymethyltransferase, O-acetylhomoserine sulfhydrylase, methylenetetrahydrofolate reductase, phosphoserine aminotransferase, phosphoserine phosphatase, serine acetyltransferase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine exporter carrier, threonine dehydratase, pyruvate oxidase, lysine exporter, biotin ligase, cysteine synthase I, cysteine synthase II, coenzyme B12-dependent methionine synthase, coenzyme B12-independent methionine synthase activity, sulfate adenylyltransferase subunit 1 and 2, phosphoadenosine-phosphosulfate reductase, ferredoxin-sulfite reductase, ferredoxin NADP reductase, 3-phosphoglycerate dehydrogenase, RXA00655 regulator, RXN2910 regulator, arginyl-tRNA synthetase, phosphoenolpyruvate

carboxylase, threonine efflux protein, serine hydroxymethyltransferase, fructose-1,6-bisphosphatase, protein of sulfate reduction RXA077, protein of sulfate reduction RXA248, protein of sulfate reduction RXA247, protein OpcA, 1-phosphofructokinase and 6-phosphofructokinase.

23. An expression vector comprising an expression cassette according to any of claims 20 to 22.

24. A genetically modified microorganism, where the genetic modification leads to an alteration or causing of the transcription rate of at least one gene compared with the wild type, and is dependent on

a) altering the specific promoter activity in the microorganism of at least one endogenous nucleic acid having promoter activity according to claim 1, which regulates the transcription of at least one endogenous gene, or

b) regulating the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 1 or by nucleic acids having promoter activity according to claim 1 with altered specific promoter activity according to embodiment a), where the genes are heterologous in relation to the nucleic acids having promoter activity.

25. The genetically modified microorganism according to claim 24, wherein the regulation of the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 1 or by nucleic acids having promoter activity according to claim 1 with altered specific promoter activity according to embodiment a), is achieved by

b1) introducing one or more nucleic acids having promoter activity according to claim 1, where appropriate with altered specific promoter activity, into the genome of the microorganism so that transcription of one or more endogenous genes takes place under the control of the introduced nucleic acid having promoter activity according to claim 1, where appropriate with altered specific promoter activity, or

b2) introducing one or more genes into the genome of the microorganism so that transcription of one or more of the introduced genes takes place under the control of the endogenous nucleic acids having promoter activity according to claim 1, where appropriate with altered specific promoter

activity, or

b3) introducing one or more nucleic acid constructs comprising a nucleic acid having promoter activity according to claim 1, where appropriate with altered specific promoter activity, and functionally linked one or more nucleic acids to be transcribed, into the microorganism.

26. The genetically modified microorganism according to claim 24 or 25 having increased or caused transcription rate of at least one gene compared with the wild type, wherein

ah) the specific promoter activity in the microorganism of endogenous nucleic acids having promoter activity according to claim 1, which regulate the transcription of endogenous genes, is increased compared with the wild type, or

bh) the transcription of genes in the microorganism is regulated by nucleic acids having promoter activity according to claim 1 or by nucleic acids having increased specific promoter activity according to embodiment ah), where the genes are heterologous in relation to the nucleic acids having promoter activity.

27. The genetically modified microorganism according to claim 26, wherein the regulation of the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 1 or by nucleic acids having promoter activity according to claim 1 with increased specific promoter activity according to embodiment a), is achieved by

bh1) introducing one or more nucleic acids having promoter activity according to claim 1, where appropriate with increased specific promoter activity, into the genome of the microorganism so that transcription of one or more endogenous genes takes place under the control of the introduced nucleic acid having promoter activity, where appropriate with increased specific promoter activity, or

bh2) introducing one or more genes into the genome of the microorganism so that transcription of one or more of the introduced genes takes place under the control of the endogenous nucleic acids having promoter activity according to claim 1, where appropriate with increased specific

promoter activity, or

bh3) introducing one or more nucleic acid constructs comprising a nucleic acid having promoter activity according to claim 1, where appropriate with increased specific promoter activity, and functionally linked one or more nucleic acids to be transcribed, into the microorganism.

28. The genetically modified microorganism according to claim 24 or 25 having reduced transcription rate of at least one gene compared with the wild type, wherein

ar) the specific promoter activity in the microorganism of at least one endogenous nucleic acid having promoter activity according to claim 1, which regulates the transcription of at least one endogenous gene, is reduced compared with the wild type, or

br) one or more nucleic acids having reduced promoter activity according to embodiment a) are introduced into the genome of the microorganism so that the transcription of at least one endogenous gene takes place under the control of the introduced nucleic acid having reduced promoter activity.

29. A genetically modified microorganism, where the genetic modification leads to an alteration or causing of the expression rate of at least one gene compared with the wild type, and is dependent on

c) altering the specific expression activity in the microorganism of at least one endogenous expression unit according to claim 2 or 3, which regulates the expression of at least one endogenous gene, compared with the wild type or

d) regulating the expression of genes in the microorganism by expression units according to claim 2 or 3 or by expression units according to claim 2 or 3 with altered specific expression activity according to embodiment a), where the genes are heterologous in relation to the expression units.

30. The genetically modified microorganism according to claim 29, wherein the regulation of the expression of genes in the microorganism by expression units according to claim 2 or 3 or by expression units according to claim 2 or 3 with altered specific expression activity according to embodiment a) is achieved by

d1) introducing one or more expression units according to claim 2 or 3, where appropriate with altered specific expression activity, into the genome of the microorganism so that expression of one or more endogenous genes takes place under the control of the introduced expression units according to claim 2 or 3, where appropriate with altered specific expression activity, or

d2) introducing one or more genes into the genome of the microorganism so that expression of one or more of the introduced genes takes place under the control of the endogenous expression units according to claim 2 or 3, where appropriate with altered specific expression activity, or

d3) introducing one or more nucleic acid constructs comprising an expression unit according to claim 2 or 3, where appropriate with altered specific expression activity, and functionally linked one or more nucleic acids to be expressed, into the microorganism.

31. The genetically modified microorganism according to claim 29 or 30 with increased or caused expression rate of at least one gene compared with the wild type, wherein

ch) the specific expression activity in the microorganism of at least one endogenous expression unit according to claim 2 or 3, which regulates the expression of the endogenous genes, is increased compared with the wild type, or

dh) the expression of genes in the microorganism is regulated by expression units according to claim 2 or 3 or by expression units according to claim 2 or 3 with increased specific expression activity according to embodiment a), where the genes are heterologous in relation to the expression units.

32. The genetically modified microorganism according to claim 31, wherein the regulation of the expression of genes in the microorganism by expression units according to claim 2 or 3 or by expression units according to claim 2 or 3 with increased specific expression activity according to embodiment a) is achieved by

dh1) introducing one or more expression units according to claim 2 or 3, where appropriate with increased specific expression activity, into the genome of the microorganism so that expression of one or more endogenous genes takes place under the control of the introduced expression unit according

to claim 2 or 3, where appropriate with increased specific expression activity, or

dh2) introducing one or more genes into the genome of the microorganism so that expression of one or more of the introduced genes takes place under the control of the endogenous expression units according to claim 2 or 3, where appropriate with increased specific expression activity, or

dh3) introducing one or more nucleic acid constructs comprising an expression unit according to claim 2 or 3, where appropriate with increased specific expression activity, and functionally linked one or more nucleic acids to be expressed, into the microorganism.

33. The genetically modified microorganism according to claim 29 or 30 with reduced expression rate of at least one gene compared with the wild type, wherein

cr) the specific expression activity in the microorganism of at least one endogenous expression unit according to claim 2 or 3, which regulates the expression of at least one endogenous gene, is reduced compared with the wild type, or

dr) one or more expression units according to claim 2 or 3 with reduced expression activity are introduced into the genome of the microorganism so that expression of at least one gene takes place under the control of the introduced expression unit according to claim 2 or 3 with reduced expression activity.

34. A genetically modified microorganism comprising an expression unit according to claim 2 or 3 and functionally linked a gene to be expressed, where the gene is heterologous in relation to the expression unit.

35. The genetically modified microorganism according to claim 34, comprising an expression cassette according to any of claims 20 to 22.

36. The genetically modified microorganism according to any of claims 24 to 35, wherein the genes are selected from the group of nucleic acids encoding a protein from the biosynthetic pathway of proteinogenic and non-proteinogenic amino acids, nucleic acids encoding a protein from the biosynthetic pathway of nucleotides and nucleosides, nucleic acid encoding a protein from the

biosynthetic pathway of organic acids, nucleic acids encoding a protein from the biosynthetic pathway of lipids and fatty acids, nucleic acids encoding a protein from the biosynthetic pathway of diols, nucleic acids encoding a protein from the biosynthetic pathway of carbohydrates, nucleic acids encoding a protein from the biosynthetic pathway of aromatic compounds, nucleic acids encoding a protein from the biosynthetic pathway of vitamins, nucleic acids encoding a protein from the biosynthetic pathway of cofactors and nucleic acids encoding a protein from the biosynthetic pathway of enzymes, where the genes may optionally comprise further regulatory elements.

37. The genetically modified microorganism according to claim 36, wherein the proteins from the biosynthetic pathway of amino acids are selected from the group of aspartate kinase, aspartate-semialdehyde dehydrogenase, diaminopimelate dehydrogenase, diaminopimelate decarboxylase, dihydrodipicolinate synthetase, dihydrodipicolinate reductase, glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, pyruvate carboxylase, triosephosphate isomerase, transcriptional regulator LuxR, transcriptional regulator LysR1, transcriptional regulator LysR2, malate-quinone oxidoreductase, glucose-6-phosphate deydrogenase, 6-phosphogluconate dehydrogenase, transketolase, transaldolase, homoserine O-acetyltransferase, cystathionine gamma-synthase, cystathionine beta-lyase, serine hydroxymethyltransferase, O-acetylhomoserine sulfhydrylase, methylenetetrahydrofolate reductase, phosphoserine aminotransferase, phosphoserine phosphatase, serine acetyltransferase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine exporter carrier, threonine dehydratase, pyruvate oxidase, lysine exporter, biotin ligase, cysteine synthase I, cysteine synthase II, coenzyme B12-dependent methionine synthase, coenzyme B12-independent methionine synthase, sulfate adenylyltransferase subunit 1 and 2, phosphoadenosine-phosphosulfate reductase, ferredoxin-sulfite reductase, ferredoxin NADP reductase, 3-phosphoglycerate dehydrogenase, RXA00655 regulator, RXN2910 regulator, arginyl-tRNA synthetase, phosphoenolpyruvate carboxylase, threonine efflux protein, serine hydroxymethyltransferase, fructose-1,6-bisphosphatase, protein of sulfate reduction RXA077, protein of sulfate reduction RXA248, protein of sulfate reduction RXA247, protein OpcA, 1-phosphofructokinase and 6-phosphofructokinase.

38. A method for preparing biosynthetic products by cultivating genetically modified microorganisms according to any of claims 24 to 37.

39. A method for preparing lysine by cultivating genetically modified microorganisms according to any of claims 24, 25, 31 or 32, wherein the genes are selected from the group of nucleic acids encoding an aspartate kinase, nucleic acids encoding an aspartate-semialdehyde dehydrogenase, nucleic acids encoding a diaminopimelate dehydrogenase, nucleic acids encoding a diaminopimelate decarboxylase, nucleic acids encoding a dihydrodipicolinate synthetase, nucleic acids encoding a dihydrodipicolinate reductase, nucleic acids encoding a glyceraldehyde-3-phosphate dehydrogenase, nucleic acids encoding a 3-phosphoglycerate kinase, nucleic acids encoding a pyruvate carboxylase, nucleic acids encoding a triosephosphate isomerase, nucleic acids encoding a transcriptional regulator LuxR, nucleic acids encoding a transcriptional regulator LysR1, nucleic acids encoding a transcriptional regulator LysR2, nucleic acids encoding a malate-quinone oxidoreductase, nucleic acids encoding a glucose-6-phosphate dehydrogenase, nucleic acids encoding a 6-phosphogluconate dehydrogenase, nucleic acids encoding a transketolase, nucleic acids encoding a transaldolase, nucleic acids encoding a lysine exporter, nucleic acids encoding a biotin ligase, nucleic acids encoding an arginyl-tRNA synthetase, nucleic acids encoding a phosphoenolpyruvate carboxylase, nucleic acids encoding a fructose-1,6-bisphosphatase, nucleic acids encoding a protein OpcA, nucleic acids encoding a 1-phosphofructokinase and nucleic acids encoding a 6-phosphofructokinase.

40. The method according to claim 39, wherein the genetically modified microorganisms have, compared with the wild type, additionally an increased activity, of at least one of the activities selected from the group of aspartate kinase activity, aspartate-semialdehyde dehydrogenase activity, diaminopimelate dehydrogenase activity, diaminopimelate decarboxylase activity, dihydrodipicolinate synthetase activity, dihydrodipicolinate reductase activity, glyceraldehyde-3-phosphate dehydrogenase activity, 3-phosphoglycerate kinase activity, pyruvate carboxylase activity, triosephosphate isomerase activity, activity of the transcriptional regulator LuxR, activity of the transcriptional regulator LysR1, activity of the transcriptional regulator LysR2, malate-quinone oxidoreductase activity, glucose-6-phosphate deydrogenase activity, 6-phosphogluconate dehydrogenase activity, transketolase activity, transaldolase activity, lysine exporter activity, arginyl-tRNA synthetase activity, phosphoenolpyruvate carboxylase activity, fructose-1,6-bisphosphatase activity, protein OpcA activity, 1-phosphofructokinase activity, 6-phosphofructokinase activity and biotin ligase activity.

41. The method according to claim 39 or 40, wherein the genetically modified microorganisms have, compared with the wild type, additionally a reduced activity, of at least one of the activities selected from the group of threonine dehydratase activity, homoserine O-acetyltransferase activity, O-acetyl-homoserine sulfhydrylase activity, phosphoenolpyruvate carboxykinase activity, pyruvate oxidase activity, homoserine kinase activity, homoserine dehydrogenase activity, threonine exporter activity, threonine efflux protein activity, asparaginase activity, aspartate decarboxylase activity and threonine synthase activity.

42. A method for preparing methionine by cultivating genetically modified microorganisms according to any of claims 24, 25, 31 or 32, wherein the genes are selected from the group of nucleic acids encoding an aspartate kinase, nucleic acids encoding an aspartate-semialdehyde dehydrogenase, nucleic acids encoding a homoserine dehydrogenase, nucleic acids encoding a glyceraldehyde-3-phosphate dehydrogenase, nucleic acids encoding a 3-phosphoglycerate kinase, nucleic acids encoding a pyruvate carboxylase, nucleic acids encoding a triosephosphate isomerase, nucleic acids encoding a homoserine O-acetyltransferase, nucleic acids encoding a cystathionine gamma-synthase, nucleic acids encoding a cystathionine beta-lyase, nucleic acids encoding a serine hydroxymethyltransferase, nucleic acids encoding an O-acetylhomoserine sulfhydrylase, nucleic acids encoding a methylenetetrahydrofolate reductase, nucleic acids encoding a phosphoserine aminotransferase, nucleic acids encoding a phosphoserine phosphatase, nucleic acids encoding a serine acetyltransferase, nucleic acids encoding a cysteine synthase I, nucleic acids encoding a cysteine synthase II, nucleic acids encoding a coenzyme B12-dependent methionine synthase, nucleic acids encoding a coenzyme B12-independent methionine synthase, nucleic acids encoding a sulfate adenylyltransferase, nucleic acids encoding a phosphoadenosine phosphosulfate reductase, nucleic acids encoding a ferredoxin-sulfite reductase, nucleic acids encoding a ferredoxin NADPH-reductase, nucleic acids encoding a ferredoxin activity, nucleic acids encoding a protein of sulfate reduction RXA077, nucleic acids encoding a protein of sulfate reduction RXA248, nucleic acids encoding a protein of sulfate reduction RXA247, nucleic acids encoding an RXA0655 regulator and nucleic acids encoding an RXN2910 regulator.

43. The method according to claim 42, wherein the genetically modified microorganisms have, compared with the wild type, additionally an increased activity, of at least one of the activities selected from the group of aspartate

kinase activity, aspartate-semialdehyde dehydrogenase activity, homoserine dehydrogenase activity, glyceraldehyde-3-phosphate dehydrogenase activity, 3-phosphoglycerate kinase activity, pyruvate carboxylase activity, triosephosphate isomerase activity, homoserine O-acetyltransferase activity, cystathionine gamma-synthase activity, cystathionine beta-lyase activity, serine hydroxymethyltransferase activity, O-acetylhomoserine sulfhydrylase activity, methylenetetrahydrofolate reductase activity, phosphoserine aminotransferase activity, phosphoserine phosphatase activity, serine acetyltransferase activity, cysteine synthase I activity, cysteine synthase II activity, coenzyme B12-dependent methionine synthase activity, coenzyme B12-independent methionine synthase activity, sulfate adenylyltransferase activity, phosphoadenosine-phosphosulfate reductase activity, ferredoxin-sulfite reductase activity, ferredoxin NADPH-reductase activity, ferredoxin activity, activity of a protein of sulfate reduction RXA077, activity of a protein of sulfate reduction RXA248, activity of a protein of sulfate reduction RXA247, activity of an RXA655 regulator and activity of an RXN2910 regulator.

44. The method according to claim 42 or 43, wherein the genetically modified microorganisms have, compared with the wild type, additionally a reduced activity, of at least one of the activities selected from the group of homoserine kinase activity, threonine dehydratase activity, threonine synthase activity, meso-diaminopimelate D-dehydrogenase activity, phosphoenolpyruvate carboxykinase activity, pyruvate oxidase activity, dihydrodipicolinate synthase activity, dihydrodipicolinate reductase activity and diaminopicolinate decarboxylase activity.

45. A method for preparing threonine by cultivating genetically modified microorganisms according to any of claims 24, 25, 31 or 32, wherein the genes are selected from the group of nucleic acids encoding an aspartate kinase, nucleic acids encoding an aspartate-semialdehyde dehydrogenase, nucleic acids encoding a glyceraldehyde-3-phosphate dehydrogenase, nucleic acids encoding a 3-phosphoglycerate kinase, nucleic acids encoding a pyruvate carboxylase, nucleic acids encoding a triosephosphate isomerase, nucleic acids encoding a homoserine kinase, nucleic acids encoding a threonine synthase, nucleic acids encoding a threonine exporter carrier, nucleic acids encoding a glucose-6-phosphate dehydrogenase, nucleic acids encoding a transaldolase, nucleic acids encoding a transketolase, nucleic acids encoding a malate-quinone oxidoreductase, nucleic acids encoding a 6-phosphogluconate dehydrogenase, nucleic acids encoding a lysine exporter, nucleic acids encoding a biotin ligase, nucleic acids encoding a

phosphoenolpyruvate carboxylase, nucleic acids encoding a threonine efflux protein, nucleic acids encoding a fructose-1,6-bisphosphatase, nucleic acids encoding an OpcA protein, nucleic acids encoding a 1-phosphofructokinase, nucleic acids encoding a 6-phosphofructokinase, and nucleic acids encoding a homoserine dehydrogenase.

46. The method according to claim 45, wherein the genetically modified microorganisms have, compared with the wild type, additionally an increased activity, of at least one of the activities selected from the group of aspartate kinase activity, aspartate-semialdehyde dehydrogenase activity, glyceraldehyde-3-phosphate dehydrogenase activity, 3-phosphoglycerate kinase activity, pyruvate carboxylase activity, triosephosphate isomerase activity, threonine synthase activity, activity of a threonine export carrier, transaldolase activity, transketolase activity, glucose-6-phosphate dehydrogenase activity, malate-quinone oxidoreductase activity, homoserine kinase activity, biotin ligase activity, phosphoenolpyruvate carboxylase activity, threonine efflux protein activity, protein OpcA activity, 1-phosphofructokinase activity, 6-phosphofructokinase activity, fructose-1-6-bisphosphatase activity, 6-phosphogluconate dehydrogenase and homoserine dehydrogenase activity.

47. The method according to claim 45 or 46, wherein the genetically modified microorganisms have, compared with the wild type, additionally a reduced activity, of at least one of the activities selected from the group of threonine dehydratase activity, homoserine O-acetyltransferase activity, serine hydroxymethyltransferase activity, O-acetylhomoserine sulfhydrylase activity, meso-diaminopimelate D-dehydrogenase activity, phosphoenolpyruvate carboxykinase activity, pyruvate oxidase activity, dihydrodipicolinate synthetase activity, dihydrodipicolinate reductase activity, asparaginase activity, aspartate decarboxylase activity, lysine exporter activity, acetolactate synthase activity, ketol-acid reductoisomerase activity, branched chain aminotransferase activity, coenzyme B12-dependent methionine synthase activity, coenzyme B12-independent methionine synthase activity, dihydroxy-acid dehydratase activity and diaminopicolinate decarboxylase activity.

48. The method according to any of claims 38 to 47, wherein the biosynthetic products are isolated and, where appropriate, purified from the cultivation medium after and/or during the cultivation step.

49. The use of the nucleic acid sequence SEQ. ID. NO. 42 as ribosome binding site in expression units which enable genes to be expressed in bacteria of the

genus Corynebacterium or Brevibacterium.

50. The use of the nucleic acid sequences SEQ. ID. NOs. 39, 40 or 41 as -10 region in expression units which enable genes to be expressed in bacteria of the genus Corynebacterium or Brevibacterium.

51. An expression unit which enables genes to be expressed in bacteria of the genus Corynebacterium or Brevibacterium, comprising the nucleic acid sequence SEQ. ID. NO. 42.

52. The expression unit according to claim 51, wherein the nucleic acid sequence SEQ. ID. NO. 42 is used as ribosome binding site.

53. An expression unit which enables genes to be expressed in bacteria of the genus Corynebacterium or Brevibacterium, comprising at least one of the nucleic acid sequences SEQ. ID. NOs. 39, 40 or 41.

54. The expression unit according to claim 53, wherein one of the nucleic acid sequences SEQ. ID. NOs. 39, 40 or 41 is used as –10 region.